



SEQUENCE LISTING

<110> Busfield, Samantha J.

<120> NOVEL MOLECULES OF THE
HERPESVIRUS-ENTRY-MEDIATOR-RELATED
PROTEIN FAMILY AND USES THEREOF

<130> MBIO98-061CP1CN1(M)

<140> 09/934,289

<141> 2001-08-21

<150> US 09/342,767

<151> 1999-06-29

<150> US 09/146,950

<151> 1998-09-03

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ctgctggagt	tcctcctgct	agctgggttc	ccgagctgcc	ggctctgagcc	tgaggc atg	299
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gag cct cct gga gac tgg ggg cct cct ccc tgg aga tcc acc ccc aga	347
Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro Arg	
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acc gac gtc ttg agg ctg gtg ctg tat ctc acc ttc ctg gga gcc ccc	395
Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala Pro	
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tgc tac gcc cca gct ctg ccg tcc tgc aag gag gac gag tac cca gtg	443
Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro Val	
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Thr	Tyr	Ile		His	Leu	Asn	Gly	Leu	Ser	Lys	Cys	Leu	Gln	Cys	Gln		
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Gln	Asp	Gly	Asp	His	Cys	Ala	Ala	Cys	Arg	Ala	Tyr	Ala	Thr	Ser	Ser		
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Pro	Gly	Gln	Arg	Val	Gln	Lys	Gly	Gly	Thr	Glu	Ser	Gln	Asp	Thr	Leu		
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Cys	Gln	Asn	Cys	Pro	Pro	Gly	Thr	Phe	Ser	Pro	Asn	Gly	Thr	Leu	Glu		
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Glu	Cys	Gln	His	Gln	Thr	Asn	Arg	Ala	Trp	Lys	Ser	Gln	Thr	Asp	Leu		
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Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro
      -5      1      5      10
Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys
      15      20      25
Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro
      30      35      40
Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys
      45      50      55
Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser
      60      65      70
Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile
      75      80      85      90
Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser
      95      100      105
Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr
      110      115      120
Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu
      125      130      135
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Leu
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aga acc gac gtc ttg agg ctg gtg ctg tat ctc acc ttc ctg gga gcc      96
Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
      20      25      30

ccc tgc tac gcc cca gct ctg ccg tcc tgc aag gag gac gag tac cca      144
Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro
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gtg ggc tcc gag tgc tgc ccc aag tgc agt cca ggt tat cgt gtg aag      192
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Glu	Ala	Cys	Gly	Glu	Leu	Thr	Gly	Thr	Val	Cys	Glu	Pro	Cys	Pro	Pro		
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ggc	acc	tac	att	gcc	cac	ctc	aat	ggc	cta	agc	aag	tgt	ctg	cag	tgc	288	
Gly	Thr	Tyr	Ile	Ala	His	Leu	Asn	Gly	Leu	Ser	Lys	Cys	Leu	Gln	Cys		
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caa	atg	tgt	gac	cca	gcc	atg	ggc	ctg	cgc	gcg	agc	cgg	aac	tgc	tcc	336	
Gln	Met	Cys	Asp	Pro	Ala	Met	Gly	Leu	Arg	Ala	Ser	Arg	Asn	Cys	Ser		
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Arg	Thr	Glu	Asn	Ala	Val	Cys	Gly	Cys	Ser	Pro	Gly	His	Phe	Cys	Ile		
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Val	Gln	Asp	Gly	Asp	His	Cys	Ala	Ala	Cys	Arg	Ala	Tyr	Ala	Thr	Ser		
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Ser	Pro	Gly	Gln	Arg	Val	Gln	Lys	Gly	Gly	Thr	Glu	Ser	Gln	Asp	Thr		
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ctg	tgt	cag	aac	tgc	ccc	ccg	ggg	acc	ttc	tct	ccc	aat	ggg	acc	ctg	528	
Leu	Cys	Gln	Asn	Cys	Pro	Pro	Gly	Thr	Phe	Ser	Pro	Asn	Gly	Thr	Leu		
				165					170					175			
gag	gaa	tgt	cag	cac	cag	acc	aac	cga	gct	tgg	aaa	agt	cag	aca	gac	576	
Glu	Glu	Cys	Gln	His	Gln	Thr	Asn	Arg	Ala	Trp	Lys	Ser	Gln	Thr	Asp		
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Leu																	

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Thr	Gly	Thr	Val	Cys	Glu	Pro	Cys	Pro	Pro	Gly	Thr	Tyr	Ile	Ala	His		
		35					40				45						
Leu	Asn	Gly	Leu	Ser	Lys	Cys	Leu	Gln	Cys	Gln	Met	Cys	Asp	Pro	Ala		
	50					55				60							
Met	Gly	Leu	Arg	Ala	Ser	Arg	Asn	Cys	Ser	Arg	Thr	Glu	Asn	Ala	Val		
65					70					75					80		
Cys	Gly	Cys	Ser	Pro	Gly	His	Phe	Cys	Ile	Val	Gln	Asp	Gly	Asp	His		

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Cys	Ala	Ala	Cys	Arg	Ala	Tyr	Ala	Thr	Ser	Ser	Pro	Gly	Gln	Arg	Val				
			100					105					110						
Gln	Lys	Gly	Gly	Thr	Glu	Ser	Gln	Asp	Thr	Leu	Cys	Gln	Asn	Cys	Pro				
		115					120					125							
Pro	Gly	Thr	Phe	Ser	Pro	Asn	Gly	Thr	Leu	Glu	Glu	Cys	Gln	His	Gln				
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1				5				10						15					
aga	acc	gac	gtc	tcg	agg	ctg	gtg	ctg	tat	ctc	acc	ttc	ctg	gga	gcc				96
Arg	Thr	Asp	Val	Ser	Arg	Leu	Val	Leu	Tyr	Leu	Thr	Phe	Leu	Gly	Ala				
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ccc	tgc	tac	gcc	cca	gct														114
Pro	Cys	Tyr	Ala	Pro	Ala														
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ctg cag tgc caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg 96
Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg
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aac tgc tcc agg aca gag aac gcc gtg tgt 126
Asn Cys Ser Arg Thr Glu Asn Ala Val Cys
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1 5 10 15
gcg tgc cgc gct tac gcc acc tcc agc ccg ggc cag agg gtg cag aag 96
Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys
20 25 30
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Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys
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Cys	Tyr	Ala	Pro	Ala	Leu	Pro	Ser	Cys	Lys	Glu	Asp	Glu	Tyr	Pro	Val		
	35					40				45							
ggc	tcc	gag	tgc	tgc	ccc	aag	tgc	agt	cca	ggt	tat	cgt	gtg	aag	gag	488	
Gly	Ser	Glu	Cys	Cys	Pro	Lys	Cys	Ser	Pro	Gly	Tyr	Arg	Val	Lys	Glu		
	50				55				60					65			
gcc	tgc	ggg	gag	ctg	acg	ggc	aca	gtg	tgt	gaa	ccc	tgc	cct	cca	ggc	536	
Ala	Cys	Gly	Glu	Leu	Thr	Gly	Thr	Val	Cys	Glu	Pro	Cys	Pro	Pro	Gly		
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acc	tac	att	gcc	cac	ctc	aat	ggc	cta	agc	aag	tgt	ctg	cag	tgc	caa	584	
Thr	Tyr	Ile	Ala	His	Leu	Asn	Gly	Leu	Ser	Lys	Cys	Leu	Gln	Cys	Gln		
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atg	tgt	gac	cca	gcc	atg	ggc	ctg	cgc	gcg	agc	cgg	aac	tgc	tcc	agg	632	
Met	Cys	Asp	Pro	Ala	Met	Gly	Leu	Arg	Ala	Ser	Arg	Asn	Cys	Ser	Arg		
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aca	gag	aac	gcc	gtg	tgt	ggc	tgc	agc	cca	ggc	cac	ttc	tgc	atc	gtc	680	
Thr	Glu	Asn	Ala	Val	Cys	Gly	Cys	Ser	Pro	Gly	His	Phe	Cys	Ile	Val		
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Gln	Asp	Gly	Asp	His	Cys	Ala	Ala	Cys	Arg	Ala	Tyr	Ala	Thr	Ser	Ser		
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Pro	Gly	Gln	Arg	Val	Gln	Lys	Gly	Gly	Thr	Glu	Ser	Gln	Asp	Thr	Leu		
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tgt	cag	aac	tgc	ccc	ccg	ggg	acc	ttc	tct	ccc	aat	ggg	acc	ctg	gag	824	
Cys	Gln	Asn	Cys	Pro	Pro	Gly	Thr	Phe	Ser	Pro	Asn	Gly	Thr	Leu	Glu		
			165					170					175				
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Glu	Cys	Gln	His	Gln	Thr	Lys	Cys	Ser	Trp	Leu	Val	Thr	Lys	Ala	Gly		
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Ala	Gly	Thr	Ser	Ser	Ser	His	Trp	Val	Trp	Trp	Phe	Leu	Ser	Gly	Ser		
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ctc	gtc	atc	gtc	att	gtt	tgc	tcc	aca	gtt	ggc	cta	atc	ata	tgt	gtg	968	
Leu	Val	Ile	Val	Ile	Val	Cys	Ser	Thr	Val	Gly	Leu	Ile	Ile	Cys	Val		
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Lys	Arg	Arg	Lys	Pro	Arg	Gly	Asp	Val	Val	Lys	Val	Ile	Val	Ser	Val		
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cag	cgg	aaa	aga	cag	gag	gca	gaa	ggt	gag	gcc	aca	gtc	att	gag	gcc	1064	
Gln	Arg	Lys	Arg	Gln	Glu	Ala	Glu	Gly	Glu	Ala	Thr	Val	Ile	Glu	Ala		

245	250	255	
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Leu Gln Ala Pro Pro Asp Val Thr Thr Val Ala Val Glu Glu Thr Ile			
260	265	270	
ccc tca ttc acg ggg agg agc cca aac cac tgacccacag actctgcacc			1162
Pro Ser Phe Thr Gly Arg Ser Pro Asn His			
275	280		
ccgacgccag agatacctgg agcgacggct gctgaaagag gctgtccacc tggcgaaacc			1222
accggagccc ggaggcttgg gggctccgcc ctgggctggc ttccgtctcc tccagtggag			1282
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cct gga gac tgg ggg cct cct ccc tgg aga tcc acc ccc aga acc gac			163
Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro Arg Thr Asp			
5	10	15	
gtc ttg agg ctg gtg ctg tat ctc acc ttt ctg gga gcc ccc tgc tac			211

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20					25					30					35			
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Ala	Pro	Ala	Leu	Pro	Ser	Cys	Lys	Glu	Asp	Glu	Tyr	Pro	Val	Gly	Ser			
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gag	tgc	tgc	ccc	aag	tgc	agt	cca	ggt	tat	cgt	gtg	aag	gag	gcc	tgc		307	
Glu	Cys	Cys	Pro	Lys	Cys	Ser	Pro	Gly	Tyr	Arg	Val	Lys	Glu	Ala	Cys			
			55					60					65					
ggg	gag	ctg	acg	ggc	aca	gtg	tgt	gaa	ccc	tgc	cct	cca	ggc	acc	tac		355	
Gly	Glu	Leu	Thr	Gly	Thr	Val	Cys	Glu	Pro	Cys	Pro	Pro	Gly	Thr	Tyr			
		70					75					80						
att	gcc	cac	ctc	aat	ggc	cta	agc	aag	tgt	ctg	cag	tgc	caa	atg	tgt		403	
Ile	Ala	His	Leu	Asn	Gly	Leu	Ser	Lys	Cys	Leu	Gln	Cys	Gln	Met	Cys			
	85					90					95							
gac	cca	gcc	atg	ggc	ctg	cgc	gcg	agc	cgg	aac	tgc	tcc	agg	aca	gag		451	
Asp	Pro	Ala	Met	Gly	Leu	Arg	Ala	Ser	Arg	Asn	Cys	Ser	Arg	Thr	Glu			
100					105					110					115			
aac	gcc	gtg	tgt	ggc	tgc	agc	cca	ggc	cac	ttc	tgc	atc	gtc	cag	gac		499	
Asn	Ala	Val	Cys	Gly	Cys	Ser	Pro	Gly	His	Phe	Cys	Ile	Val	Gln	Asp			
				120					125					130				
ggg	gac	cac	tgc	gcc	gcg	tgc	cgc	gct	tac	gcc	acc	tcc	agc	ccg	ggc		547	
Gly	Asp	His	Cys	Ala	Ala	Cys	Arg	Ala	Tyr	Ala	Thr	Ser	Ser	Pro	Gly			
			135					140					145					
cag	agg	gtg	cag	aag	gga	ggc	acc	gag	agt	cag	gac	acc	ctg	tgt	cag		595	
Gln	Arg	Val	Gln	Lys	Gly	Gly	Thr	Glu	Ser	Gln	Asp	Thr	Leu	Cys	Gln			
		150					155					160						
aac	tgc	ccc	ccg	ggg	acc	ttc	tct	ccc	aat	ggg	acc	ctg	gag	gaa	tgt		643	
Asn	Cys	Pro	Pro	Gly	Thr	Phe	Ser	Pro	Asn	Gly	Thr	Leu	Glu	Glu	Cys			
	165					170					175							
cag	cac	cag	acc	aat	tgg	cct	aat	cat	atg	tgt	gaa	aag	aag	aaa	gcc		691	
Gln	His	Gln	Thr	Asn	Trp	Pro	Asn	His	Met	Cys	Glu	Lys	Lys	Lys	Ala			
180					185				190						195			
aag	ggg	tgagcacacg	gcggcccat	cagggtcat	gtccccagcc	gtcacctctt											747	
Lys	Gly																	
ggagctctgt	caccccaagc	ctgggaggtg	gccccagagc	ttttccagga	tccgcggctc												807	
ctcccagggc	agccactgca	ggctgggggca	ggtgatgtag	tcaaggtgat	cgtctccatc												867	
cagcggaana	gacaggaggc	agaaggtgag	gccacagtca	ttgaggccct	gcaggccctt												927	
ccggacgtca	ccacggtggc	cgtggaggag	acaataccct	cattcacggg	gaggagccca												987	
aaccactgac	ccacagactc	tgcaccccg	cgccagagat	acctggagcg	acggctgctg												1047	
aaagaggctg	tccacctggc	gaaaccaccg	gagcccggag	gcttgggggc	tccgccctgg												1107	
gctggcttcc	gtctcctcca	gtggaggagg	aggtggggcc	cctgctgggg	tagagctggg												1167	
gacgccacgt	gccattccca	tggggccagt	agggcctggg	gcctctgttc	tgctgtggcc												1227	
tgagctcccc	agagtcttga	ggaggagcgc	cagttgcccc	tcgctcacag	accacacacc												1287	
cagccctcct	gggccagccc	agagggccct	tcagacccca	gctgtctgcg	cgtctgactc												1347	

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ttgtggcctc agcaggacag gccccgggca ctgcctcaca gccaaaggctg gactggggttg 1407
gctgcagtgt ggtgttttagt ggataccaca tcggaagtga ttttctaaat tggatttgaa 1467
ttcggtctct gttttctatt tgtcatgaaa cagtgtattt ggggagatgc tgtgggagga 1527
tgtaaataatc ttgtttctcc tcaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1587
aaaaaaaaa 1596

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<210> 18
<211> 197
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> (1)...(38)

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<400> 18
Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro
-35 -30 -25
Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
-20 -15 -10
Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro
-5 1 5 10
Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys
15 20 25
Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro
30 35 40
Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys
45 50 55
Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser
60 65 70
Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile
75 80 85 90
Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser
95 100 105
Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr
110 115 120
Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu
125 130 135
Glu Glu Cys Gln His Gln Thr Asn Trp Pro Asn His Met Cys Glu Lys
140 145 150
Lys Lys Ala Lys Gly
155

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<210> 19
<211> 591
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (1)...(591)

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<400> 19
atg gag cct cct gga gac tgg ggg cct cct ccc tgg aga tcc acc ccc 48
Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro
1 5 10 15

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aga acc gac gtc ttg agg ctg gtg ctg tat ctc acc ttt ctg gga gcc	96
Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala	
20 25 30	
ccc tgc tac gcc cca gct ctg ccg tcc tgc aag gag gac gag tac cca	144
Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro	
35 40 45	
gtg ggc tcc gag tgc tgc ccc aag tgc agt cca ggt tat cgt gtg aag	192
Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys	
50 55 60	
gag gcc tgc ggg gag ctg acg ggc aca gtg tgt gaa ccc tgc cct cca	240
Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro	
65 70 75 80	
ggc acc tac att gcc cac ctc aat ggc cta agc aag tgt ctg cag tgc	288
Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys	
85 90 95	
caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg aac tgc tcc	336
Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser	
100 105 110	
agg aca gag aac gcc gtg tgt ggc tgc agc cca ggc cac ttc tgc atc	384
Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile	
115 120 125	
gtc cag gac ggg gac cac tgc gcc gcg tgc cgc gct tac gcc acc tcc	432
Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser	
130 135 140	
agc ccg ggc cag agg gtg cag aag gga ggc acc gag agt cag gac acc	480
Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr	
145 150 155 160	
ctg tgt cag aac tgc ccc ccg ggg acc ttc tct ccc aat ggg acc ctg	528
Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu	
165 170 175	
gag gaa tgt cag cac cag acc aat tgg cct aat cat atg tgt gaa aag	576
Glu Glu Cys Gln His Gln Thr Asn Trp Pro Asn His Met Cys Glu Lys	
180 185 190	
aag aaa gcc aag ggg	591
Lys Lys Ala Lys Gly	
195	

<210> 20
 <211> 159
 <212> PRT
 <213> Homo sapiens

<400> 20
 Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys
 1 5 10 15

Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu
 20 25 30
 Thr Gly Thr Val Cys Glu Pro Cys Pro Pro Gly Thr Tyr Ile Ala His
 35 40 45
 Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys Gln Met Cys Asp Pro Ala
 50 55 60
 Met Gly Leu Arg Ala Ser Arg Asn Cys Ser Arg Thr Glu Asn Ala Val
 65 70 75 80
 Cys Gly Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His
 85 90 95
 Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val
 100 105 110
 Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys Gln Asn Cys Pro
 115 120 125
 Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys Gln His Gln
 130 135 140
 Thr Asn Trp Pro Asn His Met Cys Glu Lys Lys Lys Ala Lys Gly
 145 150 155

<210> 21
 <211> 38
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> (1)...(38)

<400> 21
 Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro
 -35 -30 -25
 Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
 -20 -15 -10
 Pro Cys Tyr Ala Pro Ala
 -5

<210> 22
 <211> 114
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(114)

<400> 22
 atg gag cct cct gga gac tgg ggg cct cct ccc tgg aga tcc acc ccc 48
 Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro
 1 5 10 15
 aga acc gac gtc tcg agg ctg gtg ctg tat ctc acc ttc ctg gga gcc 96
 Arg Thr Asp Val Ser Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
 20 25 30
 ccc tgc tac gcc cca gct 114
 Pro Cys Tyr Ala Pro Ala
 35

<210> 23
 <211> 34
 <212> PRT
 <213> Homo sapiens

<400> 23
 Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys Pro Lys Cys
 1 5 10 15
 Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly Thr
 20 25 30
 Val Cys

<210> 24
 <211> 42
 <212> PRT
 <213> Homo sapiens

<400> 24
 Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys
 1 5 10 15
 Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg
 20 25 30
 Asn Cys Ser Arg Thr Glu Asn Ala Val Cys
 35 40

<210> 25
 <211> 42
 <212> PRT
 <213> Homo sapiens

<400> 25
 Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His Cys Ala
 1 5 10 15
 Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys
 20 25 30
 Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys
 35 40

<210> 26
 <211> 105
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(105)

<400> 26
 tcc tgc aag gag gac gag tac cca gtg ggc tcc gag tgc tgc ccc aag 48
 Ser Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys Pro Lys
 1 5 10 15
 tgc agt cca ggt tat cgt gtg aag gag gcc tgc ggg gag ctg acg ggc 96
 Cys Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly

	20	25	30	
aca gtg tgt				105
Thr Val Cys				
35				
<210>	27			
<211>	126			
<212>	DNA			
<213>	Homo sapiens			
<220>				
<221>	CDS			
<222>	(1)...(126)			
<400>	27			
tgc cct cca ggc acc tac att gcc cac ctc aat ggc cta agc aag tgt				48
Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys				
1 5 10 15				
ctg cag tgc caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg				96
Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg				
20 25 30				
aac tgc tcc agg aca gag aac gcc gtg tgt				126
Asn Cys Ser Arg Thr Glu Asn Ala Val Cys				
35 40				
<210>	28			
<211>	126			
<212>	DNA			
<213>	Homo sapiens			
<220>				
<221>	CDS			
<222>	(1)...(126)			
<400>	28			
tgc agc cca ggc cac ttc tgc atc gtc cag gac ggg gac cac tgc gcc				48
Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His Cys Ala				
1 5 10 15				
gcg tgc cgc gct tac gcc acc tcc agc ccg ggc cag agg gtg cag aag				96
Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys				
20 25 30				
gga ggc acc gag agt cag gac acc ctg tgt				126
Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys				
35 40				
<210>	29			
<211>	2313			
<212>	DNA			
<213>	Homo sapiens			

<220>

<221> CDS

<222> (85)...(642)

<400> 29

gtcgacccac gcggtccggct gagttcctct gctggagttc atcctgctag ctgggttccc	60
gagctgccgg tctgagcctg aggc atg gag cct cct gga gac tgg ggg cct	111
Met Glu Pro Pro Gly Asp Trp Gly Pro	
1 5	
cct ccc tgg aga tcc acc ccc aga acc gac gtc tcg agg ctg gtg ctg	159
Pro Pro Trp Arg Ser Thr Pro Arg Thr Asp Val Ser Arg Leu Val Leu	
10 15 20 25	
tat ctc acc ttc ctg gga gcc ccc tgc tac gcc cca gct ctg ccg tcc	207
Tyr Leu Thr Phe Leu Gly Ala Pro Cys Tyr Ala Pro Ala Leu Pro Ser	
30 35 40	
tgc aag gag gac gag tac cca gtg ggc tcc gag tgc tgc ccc aag tgc	255
Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys Pro Lys Cys	
45 50 55	
agt cca ggt tat cgt gtg aag gag gcc tgc ggg gag ctg acg ggc aca	303
Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly Thr	
60 65 70	
gtg tgt gaa ccc tgc cct cca ggc acc tac att gcc cac ctc aat ggc	351
Val Cys Glu Pro Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn Gly	
75 80 85	
cta agc aag tgt ctg cag tgc caa atg tgt gac cca gcc atg ggc ctg	399
Leu Ser Lys Cys Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu	
90 95 100 105	
cgc gcg agc cgg aac tgc tcc agg aca gag aac gcc gtg tgt ggc tgc	447
Arg Ala Ser Arg Asn Cys Ser Arg Thr Glu Asn Ala Val Cys Gly Cys	
110 115 120	
agc cca ggc cac ttc tgc atc gtc cag gac ggg gac cac tgc gcc gcg	495
Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His Cys Ala Ala	
125 130 135	
tgc cgc gct tac gcc acc tcc agc ccg ggc cag agg gtg cag aag gga	543
Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys Gly	
140 145 150	
ggc acc gag agt cag gac acc ctg tgt cag aac tgc ccc ccg ggg acc	591
Gly Thr Glu Ser Gln Asp Thr Leu Cys Gln Asn Cys Pro Pro Gly Thr	
155 160 165	
ttc tct ccc aat ggg acc ctg gag gaa tgt cag cac cag acc aaa aag	639
Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys Gln His Gln Thr Lys Lys	
170 175 180 185	
gct tgaaggtccc accctgagcg gcaccctggt cacatgcctg cgtccaggag	692
Ala	

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agctgcaggg ctgaagcctg tgtgccccag ataaccctt ccatggggccc agacaaagcc 752
tcatacagatc tgagcttcct ggaggctcag gatgggcctt cccagaagca ggcccagagg 812
gaggctgcct ccagatcccc tgtcccctgg ggctgtgggt gtccctgaat gtcaggggcca 872
tgaggaggcc cctgggcttc aggggttggg gaaagtgaac actctgctct ttgtccacct 932
tcgggaggac accttcaaata gctgaccctg ggcccctaac tgacctgaga cttcagagct 992
tcttgggagg agctggggtc ccccagcggg gacctgggat gagcagggat ggctgcccc 1052
gggagggggc ggtggggcct tccatcctgc tctgcccctc tcgtcctctg gcccagctc 1112
agtcctgtcc atctccagct ctaaccattt ttgtcccagc actggctctc cctctacctt 1172
ctgtccttgt ctgccactgg tctcccgtgc tctggggtct ctgcaactgt ggctgcctcc 1232
cgcttctctc cctctcctct ctgccgtcct gtctcctttg cccagtctct ccttgtttct 1292
cttctcctcc ttccttctct ccacctcccc atagccgagc ttggaaaagt cagacagacc 1352
tctgagggtct catcctggag ctgccaccag cccagcctcc ctgggacctg tcttcaactgc 1412
ctggggccct gggagccagg gaggtccct gaggtgagt gaacactggg cgctgcacct 1472
gcctctccca cgtcctcggc cccactcccg caggtgcagc tggctggtga cgaaggcccg 1532
agctgggacc agcagctccc actgggtatg gtggtttctc tcagggagcc tcgtcatcgt 1592
cattgtttgc tccacagttg gcctaatacat atgtgtgaaa agaagaaagc caaggggtga 1652
tgtagtcaag gtgactcgtc ccgtccagcg gaaaagacag gaggcagaag gtgaggccac 1712
agtcattgag gccctgcagg cccctccgga cgtcaccacg gtggccgtgg aggagacaat 1772
accctcatte acgggggagga gcccaaacca ctgaccacac gactctgcac cccgacgcca 1832
gagatacctg gagcgacggc tgctgaaaga ggctgtccac ctggcgaaac caccggagcc 1892
cggaggcttg ggggctccgc cctgggctgg ctccgtctc ctccagtggg gggagaggtg 1952
gggcccctgc tggggtagag ctggggacgc cacgtgccat tcccatgggc cagtgagggc 2012
ctggggcctc tgttctgctg tggcctgagc tccccagagt cctgaggagg agcgccagtt 2072
gcccctcgtc cacagaccac acaccagcc ctctggggc agcccagagg gcccttcaga 2132
ccccagctgt ctgcgcgtct gactcttgtg gcctcagcag gacaggcccc gggcactgcc 2192
tcacagccaa ggctggactg ggttggctgc agtgtggtgt ttagtggata ccacatcgga 2252
agtgattttc taaattggat ttgaattcgg aaaaaaaaaa aaaaaaaaaa agggcgggcg 2312
c 2313

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<210> 30
<211> 186
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> (1)...(38)

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<400> 30
Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro
-35 -30 -25
Arg Thr Asp Val Ser Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
-20 -15 -10
Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro
-5 1 5 10
Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys
15 20 25
Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro
30 35 40
Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys
45 50 55
Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser
60 65 70
Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile
75 80 85 90

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Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser
95 100 105
Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr
110 115 120
Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu
125 130 135
Glu Glu Cys Gln His Gln Thr Lys Lys Ala
140 145

<210> 31
<211> 558
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(558)

<400> 31
atg gag cct cct gga gac tgg ggg cct cct ccc tgg aga tcc acc ccc 48
Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro
1 5 10 15
aga acc gac gtc tgc agg ctg gtg ctg tat ctc acc ttc ctg gga gcc 96
Arg Thr Asp Val Ser Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
20 25 30
ccc tgc tac gcc cca gct ctg ccg tcc tgc aag gag gac gag tac cca 144
Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro
35 40 45
gtg ggc tcc gag tgc tgc ccc aag tgc agt cca ggt tat cgt gtg aag 192
Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys
50 55 60
gag gcc tgc ggg gag ctg acg ggc aca gtg tgt gaa ccc tgc cct cca 240
Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro
65 70 75 80
ggc acc tac att gcc cac ctc aat ggc cta agc aag tgt ctg cag tgc 288
Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys
85 90 95
caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg aac tgc tcc 336
Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser
100 105 110
agg aca gag aac gcc gtg tgt ggc tgc agc cca ggc cac ttc tgc atc 384
Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile
115 120 125
gtc cag gac ggg gac cac tgc gcc gcg tgc cgc gct tac gcc acc tcc 432
Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser
130 135 140
agc ccg ggc cag agg gtg cag aag gga ggc acc gag agt cag gac acc 480
Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr

145		150		155		160	
ctg tgt cag aac tgc ccc ccg ggg acc ttc tct ccc aat ggg acc ctg							528
Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu							
	165			170		175	

gag gaa tgt cag cac cag acc aaa aag gct							558
Glu Glu Cys Gln His Gln Thr Lys Lys Ala							
	180			185			

<210> 32
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 32																	
Leu	Pro	Ser	Cys	Lys	Glu	Asp	Glu	Tyr	Pro	Val	Gly	Ser	Glu	Cys	Cys		
1				5					10					15			
Pro	Lys	Cys	Ser	Pro	Gly	Tyr	Arg	Val	Lys	Glu	Ala	Cys	Gly	Glu	Leu		
			20				25						30				
Thr	Gly	Thr	Val	Cys	Glu	Pro	Cys	Pro	Pro	Gly	Thr	Tyr	Ile	Ala	His		
		35					40					45					
Leu	Asn	Gly	Leu	Ser	Lys	Cys	Leu	Gln	Cys	Gln	Met	Cys	Asp	Pro	Ala		
	50					55					60						
Met	Gly	Leu	Arg	Ala	Ser	Arg	Asn	Cys	Ser	Arg	Thr	Glu	Asn	Ala	Val		
65					70					75					80		
Cys	Gly	Cys	Ser	Pro	Gly	His	Phe	Cys	Ile	Val	Gln	Asp	Gly	Asp	His		
				85					90					95			
Cys	Ala	Ala	Cys	Arg	Ala	Tyr	Ala	Thr	Ser	Ser	Pro	Gly	Gln	Arg	Val		
			100					105					110				
Gln	Lys	Gly	Gly	Thr	Glu	Ser	Gln	Asp	Thr	Leu	Cys	Gln	Asn	Cys	Pro		
		115					120					125					
Pro	Gly	Thr	Phe	Ser	Pro	Asn	Gly	Thr	Leu	Glu	Glu	Cys	Gln	His	Gln		
	130					135					140						
Thr	Lys	Lys	Ala														
145																	

<210> 33
 <211> 38
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> (1)...(38)

<400> 33																	
Met	Glu	Pro	Pro	Gly	Asp	Trp	Gly	Pro	Pro	Pro	Trp	Arg	Ser	Thr	Pro		
			-35					-30					-25				
Arg	Thr	Asp	Val	Ser	Arg	Leu	Val	Leu	Tyr	Leu	Thr	Phe	Leu	Gly	Ala		
		-20					-15					-10					
Pro	Cys	Tyr	Ala	Pro	Ala												
	-5																

<210> 34
 <211> 114

<212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(114)

<400> 34
 atg gag cct cct gga gac tgg ggg cct cct ccc tgg aga tcc acc ccc 48
 Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro
 1 5 10 15
 aga acc gac gtc tcg agg ctg gtg ctg tat ctc acc ttc ctg gga gcc 96
 Arg Thr Asp Val Ser Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
 20 25 30
 ccc tgc tac gcc cca gct 114
 Pro Cys Tyr Ala Pro Ala
 35

<210> 35
 <211> 34
 <212> PRT
 <213> Homo sapiens

<400> 35
 Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys Pro Lys Cys
 1 5 10 15
 Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly Thr
 20 25 30
 Val Cys

<210> 36
 <211> 42
 <212> PRT
 <213> Homo sapiens

<400> 36
 Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys
 1 5 10 15
 Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg
 20 25 30
 Asn Cys Ser Arg Thr Glu Asn Ala Val Cys
 35 40

<210> 37
 <211> 42
 <212> PRT
 <213> Homo sapiens

<400> 37
 Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His Cys Ala
 1 5 10 15
 Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys
 20 25 30

Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys
 35 40

<210> 38
 <211> 105
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(105)

<400> 38

tcc tgc aag gag gac gag tac cca gtg ggc tcc gag tgc tgc ccc aag 48
 Ser Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys Pro Lys
 1 5 10 15

tgc agt cca ggt tat cgt gtg aag gag gcc tgc ggg gag ctg acg ggc 96
 Cys Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly
 20 25 30

aca gtg tgt 105
 Thr Val Cys
 35

<210> 39
 <211> 126
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(126)

<400> 39

tgc cct cca ggc acc tac att gcc cac ctc aat ggc cta agc aag tgt 48
 Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys
 1 5 10 15

ctg cag tgc caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg 96
 Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg
 20 25 30

aac tgc tcc agg aca gag aac gcc gtg tgt 126
 Asn Cys Ser Arg Thr Glu Asn Ala Val Cys
 35 40

<210> 40
 <211> 126
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)...(126)

<400> 40
 tgc agc cca ggc cac ttc tgc atc gtc cag gac ggg gac cac tgc gcc 48
 Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His Cys Ala
 1 5 10 15

 gcg tgc cgc gct tac gcc acc tcc agc ccg ggc cag agg gtg cag aag 96
 Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys
 20 25 30

 gga ggc acc gag agt cag gac acc ctg tgt 126
 Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys
 35 40

 <210> 41
 <211> 1834
 <212> DNA
 <213> Homo sapiens

 <220>
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 <222> (103)...(933)

 <400> 41
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 cctgctagct gggttccccga gctgccggtc tgagcctgag gc atg gag cct cct 114
 Met Glu Pro Pro
 1

 gga gac tgg ggg cct cct ccc tgg aga tcc acc ccc aga acc gac gtc 162
 Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro Arg Thr Asp Val
 5 10 15 20

 ttg agg ctg gtg ctg tat ctc acc ttc ctg gga gcc ccc tgc tac gcc 210
 Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala Pro Cys Tyr Ala
 25 30 35

 cca gct ctg ccg tcc tgc aag gag gac gag tac cca gtg ggc tcc gag 258
 Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu
 40 45 50

 tgc tgc ccc aag tgc agt cca ggt tat cgt gtg aag gag gcc tgc ggg 306
 Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly
 55 60 65

 gag ctg acg ggc aca gtg tgt gaa ccc tgc cct cca ggc acc tac att 354
 Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro Gly Thr Tyr Ile
 70 75 80

 gcc cac ctc aat ggc cta agc aag tgt ctg cag tgc caa atg tgt gac 402
 Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys Gln Met Cys Asp
 85 90 95 100

 cca gcc atg ggc ctg cgc gcg agc cgg aac tgc tcc agg aca gag aac 450
 Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser Arg Thr Glu Asn
 105 110 115

gcc gtg tgt ggc tgc agc cca ggc cac ttc tgc atc gtc cag gac ggg Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly 120 125 130	498
gac cac tgc gcc gcg tgc cgc gct tac gcc acc tcc agc ccg ggc cag Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln 135 140 145	546
agg gtg cag aag gga ggc acc gag agt cag gac acc ctg tgt cag aac Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys Gln Asn 150 155 160	594
tgc ccc ccg ggg acc ttc tct ccc aat ggg acc ctg gag gaa tgt cag Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys Gln 165 170 175 180	642
cac cag acc aag tgc agc tgg ctg gtg acg aag gcc gga gct ggg acc His Gln Thr Lys Cys Ser Trp Leu Val Thr Lys Ala Gly Ala Gly Thr 185 190 195	690
agc agc tcc cac tgg gta tgg tgg ttt ctc tca ggg agc ctc gtc atc Ser Ser Ser His Trp Val Trp Trp Phe Leu Ser Gly Ser Leu Val Ile 200 205 210	738
gtc att gtt tgc tcc aca gtt ggc cta atc ata tgt gtg aaa aga aga Val Ile Val Cys Ser Thr Val Gly Leu Ile Ile Cys Val Lys Arg Arg 215 220 225	786
aag cca agg ggt gat gta gtc aag gtg atc gtc tcc gtc cag gta ttg Lys Pro Arg Gly Asp Val Val Lys Val Ile Val Ser Val Gln Val Leu 230 235 240	834
atc ctc ctc ccc ctc tcc ctc ccc cct cca cct tcc cac ctc ccc tct Ile Leu Leu Pro Leu Ser Leu Pro Pro Pro Pro Ser His Leu Pro Ser 245 250 255 260	882
ccc cgc tgg ggc tgg tgt ttc tgg tgt aca tgg tgg ggg ctc cca gtt Pro Arg Trp Gly Trp Cys Phe Trp Cys Thr Trp Trp Gly Leu Pro Val 265 270 275	930
ctc tgagggtcct gagtctttca agtacagcca cggtagctca ggaaagaacc Leu	983
cacccccctca aactgaaagc agtaaaatga acccgagaac ctggaggtccc agggggggcct gagcaggcag ggtctccacg attcgtgtgc tcacagcgga aaagacagga ggcagaaggt gaggccacag tcattgaggc cctgcaggcc cctccggacg tcaccacggt ggccgtggag gagacaatac cctcattcac ggggaggagc ccaaaccact gacccacaga ctctgcaccc cgacgccaga gatacctgga gcgacggctg ctgaaagagg ctgtccacct ggcgaaacca ccggagccccg gaggcttggg ggctccgccc tgggctggct tccgtctcct ccagtggagg gagaggtggg gcccctgctg gggtagagct ggggacgcca cgtgccattc ccatgggcca gtgagggcct ggggcctctg ttctgctgtg gcctgagctc cccagagtcc tgaggaggag cgccagttgc ccctcgctca cagaccacac acccagccct cctggggccag cccagagggc ccttcagacc ccagctgtct gcgctgtga ctcttgtggc ctcagcagga caggccccg gcaactgcctc acagccaagg ctggactggg ttggctgcag tgttgtgttt agtggatacc acatcggaag tgatttttcta aattggattt gaattcggct cctgttttct atttgtcatg	1043 1103 1163 1223 1283 1343 1403 1463 1523 1583 1643 1703


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aaacagtgtgta tttgggggaga tgctgtggga ggatgtaaat atcttgtttc tcctcaaaaa 1763
aaaaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1823
agggcggccg c 1834

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<210> 42
<211> 277
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> (1)...(38)

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<400> 42
Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro
-35 -30 -25
Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
-20 -15 -10
Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro
-5 1 5 10
Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys
15 20 25
Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro
30 35 40
Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys
45 50 55
Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser
60 65 70
Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile
75 80 85 90
Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser
95 100 105
Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr
110 115 120
Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu
125 130 135
Glu Glu Cys Gln His Gln Thr Lys Cys Ser Trp Leu Val Thr Lys Ala
140 145 150
Gly Ala Gly Thr Ser Ser Ser His Trp Val Trp Trp Phe Leu Ser Gly
155 160 165 170
Ser Leu Val Ile Val Ile Val Cys Ser Thr Val Gly Leu Ile Ile Cys
175 180 185
Val Lys Arg Arg Lys Pro Arg Gly Asp Val Val Lys Val Ile Val Ser
190 195 200
Val Gln Val Leu Ile Leu Leu Pro Leu Ser Leu Pro Pro Pro Pro Ser
205 210 215
His Leu Pro Ser Pro Arg Trp Gly Trp Cys Phe Trp Cys Thr Trp Trp
220 225 230
Gly Leu Pro Val Leu
235

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<210> 43
<211> 831
<212> DNA
<213> Homo sapiens

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<220>

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<221> CDS

<222> (1)...(831)

<400> 43

atg gag cct cct gga gac tgg ggg cct cct ccc tgg aga tcc acc ccc	48
Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro	
1 5 10 15	
aga acc gac gtc ttg agg ctg gtg ctg tat ctc acc ttc ctg gga gcc	96
Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala	
20 25 30	
ccc tgc tac gcc cca gct ctg ccg tcc tgc aag gag gac gag tac cca	144
Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro	
35 40 45	
gtg ggc tcc gag tgc tgc ccc aag tgc agt cca ggt tat cgt gtg aag	192
Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Ggt Tyr Arg Val Lys	
50 55 60	
gag gcc tgc ggg gag ctg acg ggc aca gtg tgt gaa ccc tgc cct cca	240
Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro	
65 70 75 80	
ggc acc tac att gcc cac ctc aat ggc cta agc aag tgt ctg cag tgc	288
Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys	
85 90 95	
caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg aac tgc tcc	336
Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser	
100 105 110	
agg aca gag aac gcc gtg tgt ggc tgc agc cca ggc cac ttc tgc atc	384
Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile	
115 120 125	
gtc cag gac ggg gac cac tgc gcc gcg tgc cgc gct tac gcc acc tcc	432
Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser	
130 135 140	
agc ccg ggc cag agg gtg cag aag gga ggc acc gag agt cag gac acc	480
Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr	
145 150 155 160	
ctg tgt cag aac tgc ccc ccg ggg acc ttc tct ccc aat ggg acc ctg	528
Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu	
165 170 175	
gag gaa tgt cag cac cag acc aag tgc agc tgg ctg gtg acg aag gcc	576
Glu Glu Cys Gln His Gln Thr Lys Cys Ser Trp Leu Val Thr Lys Ala	
180 185 190	
gga gct ggg acc agc agc tcc cac tgg gta tgg tgg ttt ctc tca ggg	624
Gly Ala Gly Thr Ser Ser Ser His Trp Val Trp Trp Phe Leu Ser Gly	
195 200 205	
agc ctc gtc atc gtc att gtt tgc tcc aca gtt ggc cta atc ata tgt	672

Ser	Leu	Val	Ile	Val	Ile	Val	Cys	Ser	Thr	Val	Gly	Leu	Ile	Ile	Cys	
210						215					220					
gtg	aaa	aga	aga	aag	cca	agg	ggg	gat	gta	gtc	aag	gtg	atc	gtc	tcc	720
Val	Lys	Arg	Arg	Lys	Pro	Arg	Gly	Asp	Val	Val	Lys	Val	Ile	Val	Ser	
225					230					235					240	
gtc	cag	gta	ttg	atc	ctc	ctc	ccc	ctc	tcc	ctc	ccc	cct	cca	cct	tcc	768
Val	Gln	Val	Leu	Ile	Leu	Leu	Pro	Leu	Ser	Leu	Pro	Pro	Pro	Pro	Ser	
				245					250					255		
cac	ctc	ccc	tct	ccc	cgc	tgg	ggc	tgg	tgt	ttc	tgg	tgt	aca	tgg	tgg	816
His	Leu	Pro	Ser	Pro	Arg	Trp	Gly	Trp	Cys	Phe	Trp	Cys	Thr	Trp	Trp	
			260					265					270			
ggg	ctc	cca	gtt	ctc												831
Gly	Leu	Pro	Val	Leu												
			275													

<210> 44
 <211> 239
 <212> PRT
 <213> Homo sapiens

<400> 44

Leu	Pro	Ser	Cys	Lys	Glu	Asp	Glu	Tyr	Pro	Val	Gly	Ser	Glu	Cys	Cys	
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Pro	Lys	Cys	Ser	Pro	Gly	Tyr	Arg	Val	Lys	Glu	Ala	Cys	Gly	Glu	Leu	
			20					25					30			
Thr	Gly	Thr	Val	Cys	Glu	Pro	Cys	Pro	Pro	Gly	Thr	Tyr	Ile	Ala	His	
			35				40					45				
Leu	Asn	Gly	Leu	Ser	Lys	Cys	Leu	Gln	Cys	Gln	Met	Cys	Asp	Pro	Ala	
	50					55				60						
Met	Gly	Leu	Arg	Ala	Ser	Arg	Asn	Cys	Ser	Arg	Thr	Glu	Asn	Ala	Val	
65					70					75					80	
Cys	Gly	Cys	Ser	Pro	Gly	His	Phe	Cys	Ile	Val	Gln	Asp	Gly	Asp	His	
				85					90					95		
Cys	Ala	Ala	Cys	Arg	Ala	Tyr	Ala	Thr	Ser	Ser	Pro	Gly	Gln	Arg	Val	
			100					105					110			
Gln	Lys	Gly	Gly	Thr	Glu	Ser	Gln	Asp	Thr	Leu	Cys	Gln	Asn	Cys	Pro	
		115					120					125				
Pro	Gly	Thr	Phe	Ser	Pro	Asn	Gly	Thr	Leu	Glu	Glu	Cys	Gln	His	Gln	
	130					135						140				
Thr	Lys	Cys	Ser	Trp	Leu	Val	Thr	Lys	Ala	Gly	Ala	Gly	Thr	Ser	Ser	
145					150					155					160	
Ser	His	Trp	Val	Trp	Trp	Phe	Leu	Ser	Gly	Ser	Leu	Val	Ile	Val	Ile	
				165					170					175		
Val	Cys	Ser	Thr	Val	Gly	Leu	Ile	Ile	Cys	Val	Lys	Arg	Arg	Lys	Pro	
			180					185					190			
Arg	Gly	Asp	Val	Val	Lys	Val	Ile	Val	Ser	Val	Gln	Val	Leu	Ile	Leu	
		195					200					205				
Leu	Pro	Leu	Ser	Leu	Pro	Pro	Pro	Pro	Ser	His	Leu	Pro	Ser	Pro	Arg	
	210					215					220					
Trp	Gly	Trp	Cys	Phe	Trp	Cys	Thr	Trp	Trp	Gly	Leu	Pro	Val	Leu		
225					230					235						

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<220>
<221> SIGNAL
<222> (1) ... (38)
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<210> 46
<211> 114
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1) ... (114)
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[illegible]

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<210> 47
<211> 34
<212> PRT
<213> Homo sapiens
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<400> 47
Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys Pro Lys Cys
1 5 10 15
Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly Thr
20 25 30
Val Cys

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<210> 48
<211> 42
<212> PRT
<213> Homo sapiens
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<400> 48
 Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys
 1 5 10 15
 Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg
 20 25 30
 Asn Cys Ser Arg Thr Glu Asn Ala Val Cys
 35 40

<210> 49
 <211> 42
 <212> PRT
 <213> Homo sapiens

<400> 49
 Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His Cys Ala
 1 5 10 15
 Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys
 20 25 30
 Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys
 35 40

<210> 50
 <211> 22
 <212> PRT
 <213> Homo sapiens

<400> 50
 Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys Gln
 1 5 10 15
 His Gln Thr Lys Cys Ser
 20

<210> 51
 <211> 25
 <212> PRT
 <213> Homo sapiens

<400> 51
 Trp Val Trp Trp Phe Leu Ser Gly Ser Leu Val Ile Val Ile Val Cys
 1 5 10 15
 Ser Thr Val Gly Leu Ile Ile Cys Val
 20 25

<210> 52
 <211> 105
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(105)

<400> 52
 tcc tgc aag gag gac gag tac cca gtg ggc tcc gag tgc tgc ccc aag
 Ser Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys Pro Lys
 1 5 10 15

48

tgc agt cca ggt tat cgt gtg aag gag gcc tgc ggg gag ctg acg ggc	96
Cys Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly	
20 25 30	

aca gtg tgt	105
Thr Val Cys	
35	

<210> 53
 <211> 126
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(126)

<400> 53	
tgc cct cca ggc acc tac att gcc cac ctc aat ggc cta agc aag tgt	48
Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys	
1 5 10 15	

ctg cag tgc caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg	96
Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg	
20 25 30	

aac tgc tcc agg aca gag aac gcc gtg tgt	126
Asn Cys Ser Arg Thr Glu Asn Ala Val Cys	
35 40	

<210> 54
 <211> 126
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(126)

<400> 54	
tgc agc cca ggc cac ttc tgc atc gtc cag gac ggg gac cac tgc gcc	48
Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His Cys Ala	
1 5 10 15	

gcg tgc cgc gct tac gcc acc tcc agc ccg ggc cag agg gtg cag aag	96
Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys	
20 25 30	

gga ggc acc gag agt cag gac acc ctg tgt	126
Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys	
35 40	

<210> 55

<211> 66
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(66)

<400> 55
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 Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys Gln
 1 5 10 15
 cac cag acc aag tgc agc 66
 His Gln Thr Lys Cys Ser
 20

<210> 56
 <211> 75
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(75)

<400> 56
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 Trp Val Trp Trp Phe Leu Ser Gly Ser Leu Val Ile Val Ile Val Cys
 1 5 10 15
 tcc aca gtt ggc cta atc ata tgt gtg 75
 Ser Thr Val Gly Leu Ile Ile Cys Val
 20 25

<210> 57
 <211> 32
 <212> DNA
 <213> Homo sapiens

<220>

<400> 57
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<210> 58
 <211> 39
 <212> DNA
 <213> Homo sapiens

<220>

<400> 58
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Input file T198sHVE1; Output File T198sHVE1.pat
Sequence length 1929

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CCACCCAGCAGGCCTGAGCCCCCTCTGCTGCCAGACCCCCCTGCTGCCACTCTCCTGCTGCTCGGGTTCTGAGGCA 158
CAGCTTGTCACACCGAGGCGGATTCTCTTTCTCTTTCTCTTTCTCTTCTGCCCCACAGCCGCAGCAATGGCGCTGAGTT 237
CCTCTGCTGGAGTTCATCCTGCTAGCTGGGTTCCCCGAGCTGCCGGTCTGAGCCTGAGGC M E P P G 5
ATG GAG CCT CCT GGA 311
D W G P P P W R S T P R T D V L R L V L 25
GAC TGG GGG CCT CCT CCC TGG AGA TCC ACC CCC AGA ACC GAC GTC TTG AGG CTG GTG CTG 371
Y L T F L G A P C Y A P A L P S C K E D 45
TAT CTC ACC TTC CTG GGA GCC CCC TGC TAC GCC CCA GCT CTG CCG TCC TGC AAG GAG GAC 431
E Y P V G S E C C P K C S P G Y R V K E 65
GAG TAC CCA GTG GGC TCC GAG TGC TGC CCC AAG TGC AGT CCA GGT TAT CGT GTG AAG GAG 491
A C G E L T G T V C E P C P P G T Y I A 85
GCC TGC GGG GAG CTG ACG GGC ACA GTG TGT GAA CCC TGC CCT CCA GGC ACC TAC ATT GCC 551
H L N G L S K C L Q C Q M C D P A M G L 105
CAC CTC AAT GGC CTA AGC AAG TGT CTG CAG TGC CAA ATG TGT GAC CCA GCC ATG GGC CTG 611
R A S R N C S R T E N A V C G C S P G H 125
CGC GCG AGC CGG AAC TGC TCC AGG ACA GAG AAC GCC GTG TGT GGC TGC AGC CCA GGC CAC 671
F C I V Q D G D H C A A C R A Y A T S S 145
TTC TGC ATC GTC CAG GAC GGG GAC CAC TGC GCC GCG TGC CGC GCT TAC GCC ACC TCC AGC 731
P G Q R V Q K G G T E S Q D T L C Q N C 165
CCG GGC CAG AGG GTG CAG AAG GGA GGC ACC GAG AGT CAG GAC ACC CTG TGT CAG AAC TGC 791
P P G T F S P N G T L E E C Q H Q T N R 185
CCC CCG GGG ACC TTC TCT CCC AAT GGG ACC CTG GAG GAA TGT CAG CAC CAG ACC AAC CGA 851
A W K S Q T D L * 194
GCT TGG AAA AGT CAG ACA GAC CTC TGA 878
GGTCTCATCCTGGAGCTGCCACCAGCCAGCCTCCCTGGGACCTGTCTTCACTGCCTGGGGCCCTGGGAGCCAGGGAGG 957
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CGTCTGACTCTTGTGGCCTCAGCAGGACAGGCCCCGGGCACTGCTCACAGCCAAGGCTGGACTGGGTGGCTGCAGTG 1747
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Figure 1



Cys
Nely
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H
ns

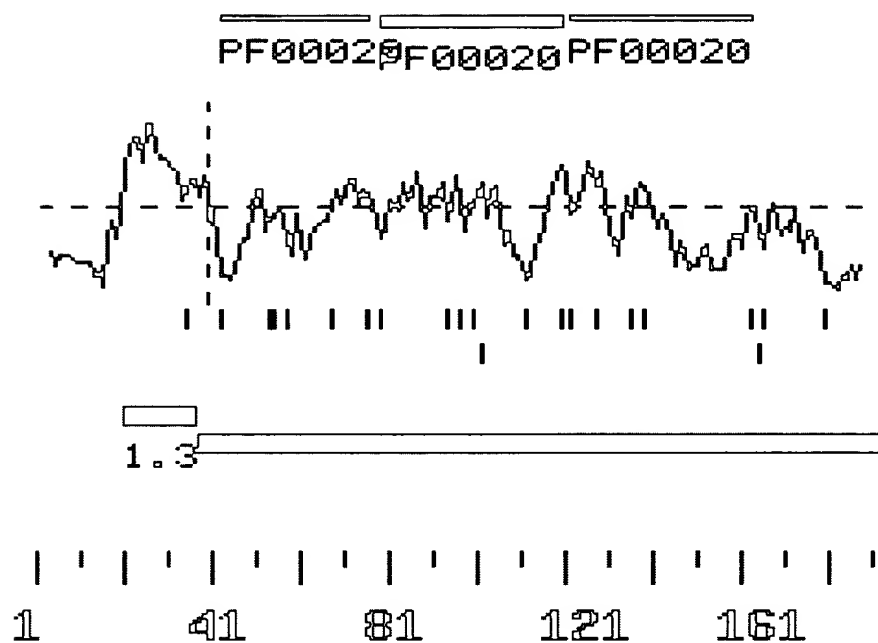


Figure 2

Input file T198sHVEM2; Output File T198sHVEM2.pat
Sequence length 1596

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S   T   P   R   T   D   V   L   R   L   V   L   Y   L   T   F   L   G   A   P   33
TCC ACC CCC AGA ACC GAC GTC TTG AGG CTG GTG CTG TAT CTC ACC TTT CTG GGA GCC CCC 205

C   Y   A   P   A   L   P   S   C   K   E   D   E   Y   P   V   G   S   E   C   53
TGC TAC GCC CCA GCT CTG CCG TCC TGC AAG GAG GAC GAG TAC CCA GTG GGC TCC GAG TGC 265

C   P   K   C   S   P   G   Y   R   V   K   E   A   C   G   E   L   T   G   T   73
TGC CCC AAG TGC AGT CCA GGT TAT CGT GTG AAG GAG GCC TGC GGG GAG CTG ACG GGC ACA 325

V   C   E   P   C   P   P   G   T   Y   I   A   H   L   N   G   L   S   K   C   93
GTG TGT GAA CCC TGC CCT CCA GGC ACC TAC ATT GCC CAC CTC AAT GGC CTA AGC AAG TGT 385

L   Q   C   Q   M   C   D   P   A   M   G   L   R   A   S   R   N   C   S   R   113
CTG CAG TGC CAA ATG TGT GAC CCA GCC ATG GGC CTG CGC GCG AGC CGG AAC TGC TCC AGG 445

T   E   N   A   V   C   G   C   S   P   G   H   F   C   I   V   Q   D   G   D   133
ACA GAG AAC GCC GTG TGT GGC TGC AGC CCA GGC CAC TTC TGC ATC GTC CAG GAC GGG GAC 505

H   C   A   A   C   R   A   Y   A   T   S   S   P   G   Q   R   V   Q   K   G   153
CAC TGC GCC GCG TGC CGC GCT TAC GCC ACC TCC AGC CCG GGC CAG AGG GTG CAG AAG GGA 565

G   T   E   S   Q   D   T   L   C   Q   N   C   P   P   G   T   F   S   P   N   173
GGC ACC GAG AGT CAG GAC ACC CTG TGT CAG AAC TGC CCC CCG GGG ACC TTC TCT CCC AAT 625

G   T   L   E   E   C   Q   H   Q   T   N   W   P   N   H   M   C   E   K   K   193
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K   A   K   G   *   198
AAA GCC AAG GGG TGA 700

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CGTGCCATTCCCATGGGCCAGTGAGGGCCTGGGGCCTCTGTTCTGCTGTGGCCTGAGCTCCCCAGAGTCCTGAGGAGGA 1253

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CTGCGCGTCTGACTCTTGTGGCCTCAGCAGGACAGGCCCCGGGCACTGCCTCACAGCCAAGGCTGGACTGGGTTGGCTG 1411

CAGTGTGGTGTTTAGTGGATACCACATCGGAAGTGATTTTCTAAATTGGATTGAATTCGGCTCCTGTTTTCTATTGT 1490

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Figure 3

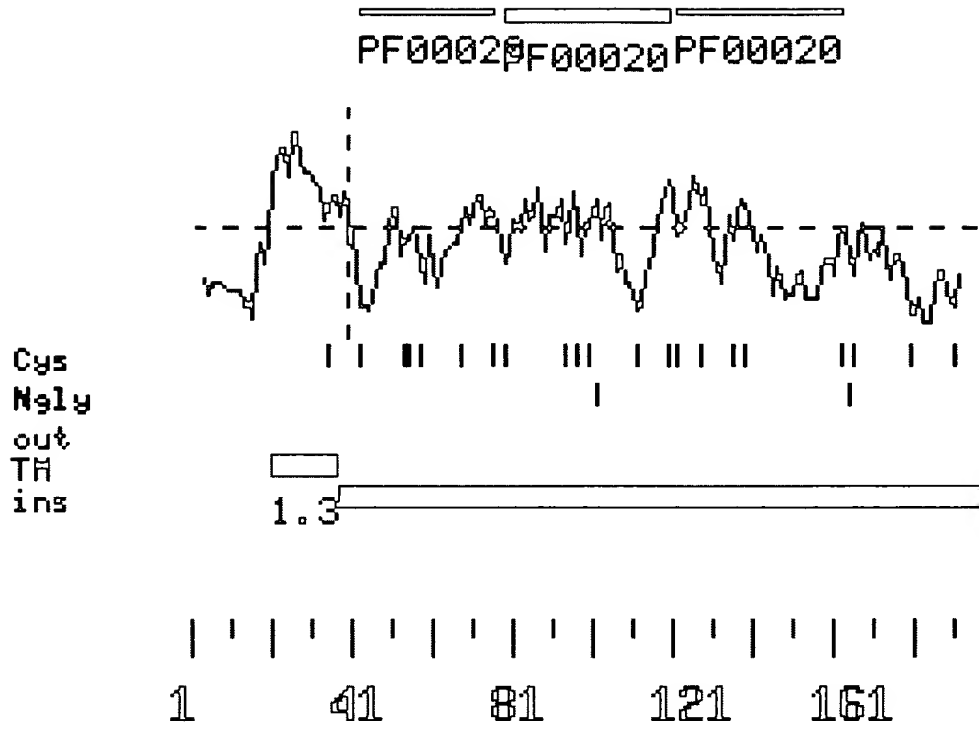


Figure 4

Input file sHVEM3; Output File sHVEM3.pat
Sequence length 2313

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      D   V   S   R   L   V   L   Y   L   T   F   L   G   A   P   C   Y   A   P   A      38
GAC GTC TCG AGG CTG GTG CTG TAT CTC ACC TTC CTG GGA GCC CCC TGC TAC GCC CCA GCT      198

      L   P   S   C   K   E   D   E   Y   P   V   G   S   E   C   C   P   K   C   S      58
CTG CCG TCC TGC AAG GAG GAC GAG TAC CCA GTG GGC TCC GAG TGC TGC CCC AAG TGC AGT      258

      P   G   Y   R   V   K   E   A   C   G   E   L   T   G   T   V   C   E   P   C      78
CCA GGT TAT CGT GTG AAG GAG GCC TGC GGG GAG CTG ACG GGC ACA GTG TGT GAA CCC TGC      318

      P   P   G   T   Y   I   A   H   L   N   G   L   S   K   C   L   Q   C   Q   M      98
CCT CCA GGC ACC TAC ATT GCC CAC CTC AAT GGC CTA AGC AAG TGT CTG CAG TGC CAA ATG      378

      C   D   P   A   M   G   L   R   A   S   R   N   C   S   R   T   E   N   A   V      118
TGT GAC CCA GCC ATG GGC CTG CGC GCG AGC CGG AAC TGC TCC AGG ACA GAG AAC GCC GTG      438

      C   G   C   S   P   G   H   F   C   I   V   Q   D   G   D   H   C   A   A   C      138
TGT GGC TGC AGC CCA GGC CAC TTC TGC ATC GTC CAG GAC GGG GAC CAC TGC GCC GCG TGC      498

      R   A   Y   A   T   S   S   P   G   Q   R   V   Q   K   G   G   T   E   S   Q      158
CGC GCT TAC GCC ACC TCC AGC CCG GGC CAG AGG GTG CAG AAG GGA GGC ACC GAG AGT CAG      558

      D   T   L   C   Q   N   C   P   P   G   T   F   S   P   N   G   T   L   E   E      178
GAC ACC CTG TGT CAG AAC TGC CCC CCG GGG ACC TTC TCT CCC AAT GGG ACC CTG GAG GAA      618

      C   Q   H   Q   T   K   K   A   *
TGT CAG CAC CAG ACC AAA AAG GCT TGA      187
                                           645

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GCCCAGAGGGAGGCTGCCTCCAGATCCCTGTCCCTTGGGGCTGTGGGTGTCCCTGAATGTCAGGGCCATGGGAGGGCC 882
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```

Figure 5

GTCGACCCACGCGTCCGCACAGCCGAGCAATGGCGCTGAGTTCCTCTGCTGGAGTTCATCCTGCTAGCTGGGTTCCCG 79

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T P R T D V L R L V L Y L T F L G A P C 34
ACC CCC AGA ACC GAC GTC TTG AGG CTG GTG CTG TAT CTC ACC TTC CTG GGA GCC CCC TGC 204

Y A P A L P S C K E D E Y P V G S E C C 54
TAC GCC CCA GCT CTG CCG TCC TGC AAG GAG GAC GAG TAC CCA GTG GGC TCC GAG TGC TGC 264

P K C S P G Y R V K E A C G E L T G T V 74
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C E P C P P G T Y I A H L N G L S K C L 94
TGT GAA CCC TGC CCT CCA GGC ACC TAC ATT GCC CAC CTC AAT GGC CTA AGC AAG TGT CTG 384

Q C Q M C D P A M G L R A S R N C S R T 114
CAG TGC CAA ATG TGT GAC CCA GCC ATG GGC CTG CGC GCG AGC CGG AAC TGC TCC AGG ACA 444

E N A V C G C S P G H F C I V Q D G D H 134
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C A A C R A Y A T S S P G Q R V Q K G G 154
TGC GCC GCG TGC CGC GCT TAC GCC ACC TCC AGC CCG GGC CAG AGG GTG CAG AAG GGA GGC 564

T E S Q D T L C Q N C P P G T F S P N G 174
ACC GAG AGT CAG GAC ACC CTG TGT CAG AAC TGC CCC CCG GGC ACC TTC TCT CCC AAT GGC 624

T L E E C Q H Q T K C S W L V T K A G A 194
ACC CTG GAG GAA TGT CAG CAC CAG ACC AAG TGC AGC TGG CTG GTG ACG AAG GCC GGA GCT 684

G T S S S H W V W W F L S G S L V I V I 214
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V C S T V G L I I C V K R R K P R G D V 234
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P V L * 278
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Figure 7



Cys
Ngly
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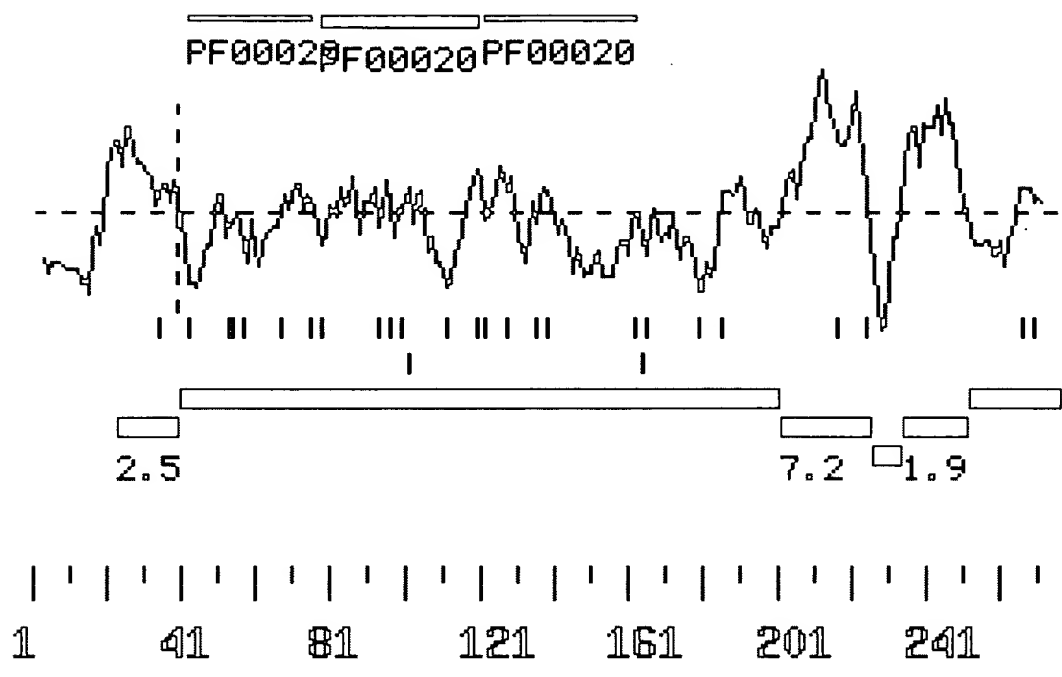


Figure 8

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Figure 9C

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2321
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2801
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2881

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2904

Figure 9D

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shVEM_2_a.a.		GTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDT	
shVEM_3_a.a.		GTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDT	
mHVEM_2_a.a.		GTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDT	
mHVEM__pub.__a.a.		GTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDT	
shVEM_1_a.a.	161	LCQNCPPGTFSPNGTLEECQHQTNRWKSQTDL-----	240
shVEM_2_a.a.		LCQNCPPGTFSPNGTLEECQHQTNRWPNHMCEKKKAG-----	
shVEM_3_a.a.		LCQNCPPGTFSPNGTLEECQHQTTKA-----	
mHVEM_2_a.a.		LCQNCPPGTFSPNGTLEECQHQTCKSWLVTKAGAGTSSSHVWVWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS	
mHVEM__pub.__a.a.		LCQNCPPGTFSPNGTLEECQHQTCKSWLVTKAGAGTSSSHVWVWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS	
shVEM_1_a.a.	241	-----	283
shVEM_2_a.a.		-----	
shVEM_3_a.a.		-----	
mHVEM_2_a.a.		VQVLILLPLSLPPPSHLPSRWGWCFTWWGLPVL-----	
mHVEM__pub.__a.a.		VQRKRQEAEGEATVIEALQAPPDVTTVAVEETIPSFTGRSPNH	

Figure 10